

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

5 (i) APPLICANT: Adams, Camilia W.  
Ashkenazi, Avi J.  
Chuntharapai, Anan  
Kim, Kyung J.

10 (ii) TITLE OF INVENTION: Apo-2 Receptor

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:  
15 (A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 1 DNA Way  
(C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
20 (F) ZIP: 94080

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
30 (B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Marschang, Diane L.  
35 (B) REGISTRATION NUMBER: 35,600  
(C) REFERENCE/DOCKET NUMBER: P1101R2

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(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 650/225-5416  
40 (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
45 (A) LENGTH: 411 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

50 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg  
1 5 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro  
20 25 30

55 Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val  
35 40 45

60 Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp  
50 55 60

	Leu	Ala	Pro	Gln	Gln	Arg	Ala	Ala	Pro	Gln	Gln	Lys	Arg	Ser	Ser	
					65					70					75	
5	Pro	Ser	Glu	Gly	Leu	Cys	Pro	Pro	Gly	His	His	Ile	Ser	Glu	Asp	
					80					85					90	
	Gly	Arg	Asp	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr	
					95					100					105	
10	His	Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp	
					110					115					120	
	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	Arg	Asn	Thr	
					125					130					135	
15	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	Glu	Glu	Asp	Ser	Pro	
					140					145					150	
	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val	
20					155					160					165	
	Lys	Val	Gly	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His	
					170					175					180	
25	Lys	Glu	Ser	Gly	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val	
					185					190					195	
	Leu	Ile	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys	
					200					205					210	
30	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Asp	
					215					220					225	
	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	Gly	Ala	Glu	Asp	
35					230					235					240	
	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	Leu	Gln	Pro	Thr	Gln	Val	
					245					250					255	
40	Pro	Glu	Gln	Glu	Met	Glu	Val	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly	
					260					265					270	
	Val	Asn	Met	Leu	Ser	Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu	Pro	
					275					280					285	
45	Ala	Glu	Ala	Glu	Arg	Ser	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala	
					290					295					300	
	Asn	Glu	Gly	Asp	Pro	Thr	Glu	Thr	Leu	Arg	Gln	Cys	Phe	Asp	Asp	
50					305					310					315	
	Phe	Ala	Asp	Leu	Val	Pro	Phe	Asp	Ser	Trp	Glu	Pro	Leu	Met	Arg	
					320					325					330	
55	Lys	Leu	Gly	Leu	Met	Asp	Asn	Glu	Ile	Lys	Val	Ala	Lys	Ala	Glu	
					335					340					345	
	Ala	Ala	Gly	His	Arg	Asp	Thr	Leu	Tyr	Thr	Met	Leu	Ile	Lys	Trp	
60					350					355					360	

Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp  
 365 370 375

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu  
 5 380 385 390

Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn  
 395 400 405

Ala Asp Ser Ala Xaa Ser  
 10 410 411

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

GCGCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC 100

CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145  
 Met Glu  
 1

CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184  
 Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg  
 5 10 15

AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223  
~~Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala~~  
 20 25

AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262  
 Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val  
 30 35 40

GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301  
 Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala  
 45 45 50

CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340  
 Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala  
 50 55 60 65

GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379  
 Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu  
 70 75 80

TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418  
 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp  
 85 90

	TGC	ATC	TCC	TGC	AAA	TAT	GGA	CAG	GAC	TAT	AGC	ACT	CAC	457
	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr	His	
		95					100					105		
5	TGG	AAT	GAC	CTC	CTT	TTC	TGC	TTG	CGC	TGC	ACC	AGG	TGT	496
	Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	
				110				115						
10	GAT	TCA	GGT	GAA	GTG	GAG	CTA	AGT	CCC	TGC	ACC	ACG	ACC	535
	Asp	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	
		120				125					130			
15	AGA	AAC	ACA	GTG	TGT	CAG	TGC	GAA	GAA	GGC	ACC	TTC	CGG	574
	Arg	Asn	Thr	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	
			135					140					145	
20	GAA	GAA	GAT	TCT	CCT	GAG	ATG	TGC	CGG	AAG	TGC	CGC	ACA	613
	Glu	Glu	Asp	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	
					150					155				
25	GGG	TGT	CCC	AGA	GGG	ATG	GTC	AAG	GTC	GGT	GAT	TGT	ACA	652
	Gly	Cys	Pro	Arg	Gly	Met	Val	Lys	Val	Gly	Asp	Cys	Thr	
		160				165						170		
30	CCC	TGG	AGT	GAC	ATC	GAA	TGT	GTC	CAC	AAA	GAA	TCA	GGC	691
	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His	Lys	Glu	Ser	Gly	
				175					180					
35	ATC	ATC	ATA	GGA	GTC	ACA	GTT	GCA	GCC	GTA	GTC	TTG	ATT	730
	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val	Leu	Ile	
		185				190					195			
40	GTG	GCT	GTG	TTT	GTT	TGC	AAG	TCT	TTA	CTG	TGG	AAG	AAA	769
	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys	
			200				205						210	
45	GTC	CTT	CCT	TAC	CTG	AAA	GGC	ATC	TGC	TCA	GGT	GGT	GGT	808
	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	
					215					220				
50	GGG	GAC	CCT	GAG	CGT	GTG	GAC	AGA	AGC	TCA	CAA	CGA	CCT	847
	Gly	Asp	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	
		225					230					235		
55	GGG	GCT	GAG	GAC	AAT	GTC	CTC	AAT	GAG	ATC	GTG	AGT	ATC	886
	Gly	Ala	Glu	Asp	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	
				240				245						
60	TTG	CAG	CCC	ACC	CAG	GTC	CCT	GAG	CAG	GAA	ATG	GAA	GTC	925
	Leu	Gln	Pro	Thr	Gln	Val	Pro	Glu	Gln	Glu	Met	Glu	Val	
		250				255					260			
65	CAG	GAG	CCA	GCA	GAG	CCA	ACA	GGT	GTC	AAC	ATG	TTG	TCC	964
	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly	Val	Asn	Met	Leu	Ser	
			265				270						275	
70	CCC	GGG	GAG	TCA	GAG	CAT	CTG	CTG	GAA	CCG	GCA	GAA	GCT	1003
	Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu	Pro	Ala	Glu	Ala	
					280					285				

GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT 1042  
 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn  
 290 295 300

5 GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT 1081  
 Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp  
 305 310

10 GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG 1120  
 Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro  
 315 320 325

15 CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159  
 Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys  
 330 335 340

20 GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198  
 Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu  
 345 350

TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237  
 Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg  
 355 360 365

25 GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276  
 Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr  
 370 375

30 CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315  
 Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His  
 380 385 390

35 TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354  
 Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn  
 395 400 405

GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400  
 Ala Asp Ser Ala Xaa Ser  
 410 411

40 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450

AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500

45 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAAGTT TTCCTGCAC 1550

TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

50 GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA 1650

TTGTTTTTAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700

TTGGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAAG 1750

55 GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 70 base pairs  
 (B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50  
GCTAAAGCTG AGGCAGCGGG 70

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 930 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36  
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe  
1 5 10

TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75  
Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile  
15 20 25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114  
Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met  
30 35

	GCC	GAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GGA	GGT	GTG	GAA	153
	Ala	Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Glu	
	40						45					50		
5	CGG	CCG	GGG	GGG	TCC	CTG	AGA	CTC	TCC	TGT	GCA	GCC	TCT	192
	Arg	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	
			55						60					
10	GGA	TTC	ACC	TTT	GAT	GAT	TAT	GGC	ATG	AGC	TGG	GTC	CGC	231
	Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Gly	Met	Ser	Trp	Val	Arg	
	65				70						75			
15	CAA	GCT	CCA	GGG	AAG	GGG	CTG	GAG	TGG	GTC	TCT	GGT	ATT	270
	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Gly	Ile	
		80					85						90	
20	AAT	TGG	AAT	GGT	GGT	AGC	ACA	GGA	TAT	GCA	GAC	TCT	GTG	309
	Asn	Trp	Asn	Gly	Gly	Ser	Thr	Gly	Tyr	Ala	Asp	Ser	Val	
				95						100				
25	AAG	GGC	CGA	GTC	ACC	ATC	TCC	AGA	GAC	AAC	GCC	AAG	AAC	348
	Lys	Gly	Arg	Val	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	
	105						110					115		
30	TCC	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCC	GAG	GAC	387
	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
				120					125					
35	ACG	GCC	GTA	TAT	TAC	TGT	GCG	AAA	ATC	CTG	GGT	GCC	GGA	426
	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Ile	Leu	Gly	Ala	Gly	
	130					135					140			
40	CGG	GGC	TGG	TAC	TTC	GAT	CTC	TGG	GGG	AAG	GGG	ACC	ACG	465
	Arg	Gly	Trp	Tyr	Phe	Asp	Leu	Trp	Gly	Lys	Gly	Thr	Thr	
			145				150						155	
45	GTC	ACC	GTC	TCG	AGT	GGT	GGA	GGC	GGT	TCA	GGC	GGA	GGT	504
	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
					160					165				
50	GGC	AGC	GGC	GGT	GGC	GGA	TCG	TCT	GAG	CTG	ACT	CAG	GAC	543
	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Glu	Leu	Thr	Gln	Asp	
	170						175					180		
55	CCT	GCT	GTG	TCT	GTG	GCC	TTG	GGA	CAG	ACA	GTC	AGG	ATC	582
	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln	Thr	Val	Arg	Ile	
				185					190					
60	ACA	TGC	CAA	GGA	GAC	AGC	CTC	AGA	AGC	TAT	TAT	GCA	AGC	621
	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala	Ser	
	195					200					205			
65	TGG	TAC	CAG	CAG	AAG	CCA	GGA	CAG	GCC	CCT	GTA	CTT	GTC	660
	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	
			210				215						220	
70	ATC	TAT	GGT	AAA	AAC	AAC	CGG	CCC	TCA	GGG	ATC	CCA	GAC	699
	Ile	Tyr	Gly	Lys	Asn	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	
				225						230				

CGA TTC TCT GGC TCC AGC TCA GGA AAC ACA GCT TCC TTG 738  
 Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu  
 235 240 245

5 ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG GCT GAC TAT 777  
 Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr  
 250 255

10 TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC CAT GTG GTA 816  
 Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val  
 260 265 270

15 TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT GCG GCC 855  
 Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala  
 275 280 285

20 GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA GAA CAA AAA 894  
 Ala His His His His His His Gly Ala Ala Glu Gln Lys  
 290 295

CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA TAG 930  
 Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala  
 300 305 309

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 939 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36  
 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe  
 1 5 10

40 TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75  
 Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile  
 15 20 25

45 CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114  
 Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met  
 30 35

50 GCC GGG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTC 153  
 Ala Gly Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val  
 40 45 50

55 CAG CCT GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT 192  
 Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser  
 55 60

GGA TTC ACC TTT AGT AGC TAT TGG ATG AGC TGG GTC CGC 231  
 Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val Arg  
 65 70 75



	CAG	GCT	CCA	GGG	AAG	GGG	CTG	GAG	TGG	GTG	GCC	AAC	ATA	270
	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Asn	Ile	
			80					85					90	
5	AAG	CAA	GAT	GGA	AGT	GAG	AAA	TAC	TAT	GTG	GAC	TCT	GTG	309
	Lys	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	
				95					100					
10	AAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA	GAC	AAC	GCC	AAG	AAC	348
	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	
		105					110					115		
15	TCA	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCC	GAG	GAC	387
	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
				120					125					
20	ACG	GCT	GTG	TAT	TAC	TGT	GCG	AGA	GAT	CTT	TTA	AAG	GTC	426
	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Leu	Leu	Lys	Val	
		130				135					140			
25	AAG	GGC	AGC	TCG	TCT	GGG	TGG	TTC	GAC	CCC	TGG	GGG	AGA	465
	Lys	Gly	Ser	Ser	Ser	Gly	Trp	Phe	Asp	Pro	Trp	Gly	Arg	
			145				150						155	
30	GGG	ACC	ACG	GTC	ACC	GTC	TCG	AGT	GGT	GGA	GGC	GGT	TCA	504
	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	
					160					165				
35	GGC	GGA	GGT	GGT	AGC	GGC	GGT	GGC	GGA	TCG	TCT	GAG	CTG	543
	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Glu	Leu	
		170				175						180		
40	ACT	CAG	GAC	CCT	GCT	GTG	TCT	GTG	GCC	TTG	GGA	CAG	ACA	582
	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln	Thr	
				185					190					
45	GTC	AGG	ATC	ACA	TGC	CAA	GGA	GAC	AGC	CTC	AGA	AGC	TAT	621
	Val	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	
		195				200					205			
50	TAT	GCA	AGC	TGG	TAC	CAG	CAG	AAG	CCA	GGA	CAG	GCC	CCT	660
	Tyr	Ala	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	
			210					215					220	
55	GTA	CTT	GTC	ATC	TAT	GGT	AAA	AAC	AAC	CGG	CCC	TCA	GGG	699
	Val	Leu	Val	Ile	Tyr	Gly	Lys	Asn	Asn	Arg	Pro	Ser	Gly	
					225					230				
60	ATC	CCA	GAC	CGA	TTC	TCT	GGC	TCC	AGC	TCA	GGA	AAC	ACA	738
	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	Ser	Gly	Asn	Thr	
		235					240					245		
65	GCT	TCC	TTG	ACC	ATC	ACT	GGG	GCT	CAG	GCG	GAA	GAT	GAG	777
	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu	Asp	Glu	
				250				255						
70	GCT	GAC	TAT	TAC	TGT	AAC	TCC	CGG	GAC	AGC	AGT	GGT	AAC	816
	Ala	Asp	Tyr	Tyr	Cys	Asn	Ser	Arg	Asp	Ser	Ser	Gly	Asn	
		260				265					270			

CAT GTG GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA 855  
 His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu  
 275 280 285

5 GGT GCG GCC GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA 894  
 Gly Ala Ala Ala His His His His His His Gly Ala Ala  
 290 295

10 GAA CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC 933  
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala  
 300 305 310

GCA TAG 939

Ala

15 312

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 933 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36  
 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe  
 30 1 5 10

TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75  
 Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile  
 15 20 25

35 CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114  
~~Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met~~  
 30 35

40 GCC CAG GTG CAG CTG GTG CAG TCT GGG GGA GGC GTG GTC 153  
 Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val  
 40 45 50

45 CAG CCT GGG CGG TCC CTG AGA CTC TCC TGT GCA GCT TCT 192  
 Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser  
 55 60

GGG TTC ATT TTC AGT AGT TAT GGG ATG CAC TGG GTC CGC 231  
 Gly Phe Ile Phe Ser Ser Tyr Gly Met His Trp Val Arg  
 50 65 70 75

CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG GCA GGT ATT 270  
 Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile  
 80 85 90

55 TTT TAT GAT GGA GGT AAT AAA TAC TAT GCA GAC TCC GTG 309  
 Phe Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val  
 95 100

	AAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA	GAC	AAT	TCC	AAG	AAC	348
	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	
		105					110					115		
5	ACG	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCT	GAG	GAC	387
	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
				120					125					
10	ACG	GCT	GTG	TAT	TAC	TGT	GCG	AGA	GAT	AGG	GGC	TAC	TAC	426
	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Arg	Gly	Tyr	Tyr	
		130				135					140			
15	TAC	ATG	GAC	GTC	TGG	GGC	AAA	GGG	ACC	ACG	GTC	ACC	GTC	465
	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	
			145				150						155	
20	TCC	TCA	GGT	GGA	GGC	GGT	TCA	GGC	GGA	GGT	GGC	TCT	GGC	504
	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	
					160					165				
25	GGT	GGC	GGA	TCG	CAG	TCT	GTG	TTG	ACG	CAG	CCG	CCC	TCA	543
	Gly	Gly	Gly	Ser	Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	
		170				175						180		
30	GTG	TCT	GGG	GCC	CCA	GGA	CAG	AGG	GTC	ACC	ATC	TCC	TGC	582
	Val	Ser	Gly	Ala	Pro	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys	
				185				190						
35	ACT	GGG	AGA	AGC	TCC	AAC	ATC	GGG	GCA	GGT	CAT	GAT	GTA	621
	Thr	Gly	Arg	Ser	Ser	Asn	Ile	Gly	Ala	Gly	His	Asp	Val	
		195				200					205			
40	CAC	TGG	TAC	CAG	CAA	CTT	CCA	GGA	ACA	GCC	CCC	AAA	CTC	660
	His	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	
			210					215					220	
45	CTC	ATC	TAT	GAT	GAC	AGC	AAT	CGG	CCC	TCA	GGG	GTC	CCT	699
	Leu	Ile	Tyr	Asp	Asp	Ser	Asn	Arg	Pro	Ser	Gly	Val	Pro	
					225					230				
50	GAC	CGA	TTC	TCT	GGC	TCC	AGG	TCT	GGC	ACC	TCA	GCC	TCC	738
	Asp	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Thr	Ser	Ala	Ser	
		235					240					245		
55	CTG	GCC	ATC	ACT	GGG	CTC	CAG	GCT	GAA	GAT	GAG	GCT	GAT	777
	Leu	Ala	Ile	Thr	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	
				250				255						
60	TAT	TAC	TGC	CAG	TCC	TAT	GAC	AGC	AGC	CTG	AGG	GGT	TCG	816
	Tyr	Tyr	Cys	Gln	Ser	Tyr	Asp	Ser	Ser	Leu	Arg	Gly	Ser	
		260				265					270			
65	GTA	TTC	GGC	GGA	GGG	ACC	AAG	GTC	ACT	GTC	CTA	GGT	GCG	855
	Val	Phe	Gly	Gly	Gly	Thr	Lys	Val	Thr	Val	Leu	Gly	Ala	
			275				280						285	
70	GCC	GCA	CAT	CAT	CAT	CAC	CAT	CAC	GGG	GCC	GCA	GAA	CAA	894
	Ala	Ala	His	His	His	His	His	His	Gly	Ala	Ala	Glu	Gln	
					290				295					

AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA 930  
 Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala  
 300 305 310

5 TAG 933

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 309 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

15 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile  
 1 5 10 15  
 20 Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro  
 20 20 25 30  
 Phe Tyr Ala Ala Gln Pro Ala Met Ala Glu Val Gln Leu Val Gln  
 35 40 45  
 25 Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser  
 50 55 60  
 Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp  
 65 70 75  
 30 Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile  
 80 85 90  
 35 Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly  
 95 100 105  
 Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 110 115 120  
 40 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 125 130 135  
 Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp  
 140 145 150  
 45 Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser  
 155 160 165  
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln  
 170 175 180  
 50 Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr  
 185 190 195  
 55 Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln  
 200 205 210  
 Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn  
 215 220 225  
 60

	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	Ser	
					230					235					240	
5	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu	Asp	
					245					250					255	
	Glu	Ala	Asp	Tyr	Tyr	Cys	Asn	Ser	Arg	Asp	Ser	Ser	Gly	Asn	His	
					260					265					270	
10	Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Ala	Ala	
					275					280					285	
	Ala	His	His	His	His	His	His	Gly	Ala	Ala	Glu	Gln	Lys	Leu	Ile	
					290					295					300	
15	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala							
					305				309							

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

	Met	Thr	Met	Ile	Thr	Pro	Ser	Phe	Gly	Ala	Phe	Phe	Leu	Glu	Ile	
	1				5					10					15	
30	Phe	Asn	Val	Lys	Lys	Leu	Leu	Phe	Ala	Ile	Pro	Leu	Val	Val	Pro	
					20					25					30	
35	Phe	Tyr	Ala	Ala	Gln	Pro	Ala	Met	Ala	Gly	Val	Gln	Leu	Val	Glu	
					35					40					45	
	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	
					50					55					60	
40	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Trp	Met	Ser	Trp	
					65					70					75	
	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Asn	Ile	
					80					85					90	
45	Lys	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys	Gly	
					95					100					105	
	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu	
50					110					115					120	
	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
					125					130					135	
55	Ala	Arg	Asp	Leu	Leu	Lys	Val	Lys	Gly	Ser	Ser	Ser	Gly	Trp	Phe	
					140					145					150	
	Asp	Pro	Trp	Gly	Arg	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	
60					155					160					165	

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu  
 170 175 180  
 5 Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val  
 185 190 195  
 Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser  
 200 205 210  
 10 Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr  
 215 220 225  
 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly  
 230 235 240  
 15 Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln  
 245 250 255  
 Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser  
 260 265 270  
 Gly Asn His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu  
 275 280 285  
 25 Gly Ala Ala Ala His His His His His His Gly Ala Ala Glu Gln  
 290 295 300  
 Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala  
 305 310 312

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

40 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile  
 1 5 10 15  
 Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro  
 20 25 30  
 45 Phe Tyr Ala Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln  
 35 40 45  
 50 Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser  
 50 55 60  
 Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr Gly Met His Trp  
 65 70 75  
 55 Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile  
 80 85 90  
 Phe Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly  
 95 100 105

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu  
110 115 120

5 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
125 130 135

Ala Arg Asp Arg Gly Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly  
140 145 150

10 Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly  
155 160 165

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro  
170 175 180

15 Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr  
185 190 195

20 Gly Arg Ser Ser Asn Ile Gly Ala Gly His Asp Val His Trp Tyr  
200 205 210

Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asp  
215 220 225

25 Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Arg  
230 235 240

Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu  
245 250 255

30 Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Arg  
260 265 270

35 Gly Ser Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala  
275 280 285

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Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu  
290 295 300

40 Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala  
305 310

## (2) INFORMATION FOR SEQ ID NO:12:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGCGGATAAC AATTCACAC AGG 23

55

## (2) INFORMATION FOR SEQ ID NO:13:

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

5

GTCGTCTTTC CAGACGGTAG T 21

(2) INFORMATION FOR SEQ ID NO:14:

10

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Ala	Asp	Pro	Asn	Arg	Phe	Arg	Gly	Lys	Asp	Leu
1				5				10		12	

20

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